

SEP 16 2003

TECH CEN



1600

RAW SEQUENCE LISTING

DATE: 09/11/2003

PATENT APPLICATION: US/09/973,382C

TIME: 11:29:04

Input Set : A:\D6230SEQ.txt

Output Set: N:\CRF4\09112003\I973382C.raw

2 <110> APPLICANT: Heston, Warren D.W.
3 O'Keefe, Denise S.
5 <120> TITLE OF INVENTION: DNA Encoding the Prostate-Specific Membrane
6 Antigen-Like Gene and Uses Thereof
8 <130> FILE REFERENCE: D6230
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/973,382C
11 <141> CURRENT FILING DATE: 2001-10-09
13 <150> PRIOR APPLICATION NUMBER: PCT/US00/09417
14 <151> PRIOR FILING DATE: 2000-04-09
16 <160> NUMBER OF SEQ ID NOS: 38
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 1992
20 <212> TYPE: DNA
21 <213> ORGANISM: Homo sapiens
23 <220> FEATURE:
24 <223> OTHER INFORMATION: cDNA sequence of PSMA-like gene
26 <400> SEQUENCE: 1
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29 gatgtccttt tttgtaggcc taatgacaaa aggttgaaga taaagttcta 150
30 gtactcattt aagtgttaata ttgaaaattg atattaccaa atctggaaca 200
31 accaatttta aataaggaaa gaaagacact gtgttttcta ggtaaaaaat 250
32 gccagctggc caggggccaa aggagtcatt ctctactcag accctgctga 300
33 ctactttgct cctgggggtga agtcctatcc agacggttgg aatcttctg 350
34 gaggtggtgt ccagcgtgga aatatactaa atctgaatgg tgcaggagac 400
35 cctctcacac caggttaccc agcaaatgaa tacgcttata ggcattggaat 450
36 tgcagaggct gttggtcttc caagtattcc tgttcatcca gttggatact 500
37 atgatgcaca gaagtccta gaaaaaatgg gtggctcagc accaccagat 550
38 agcagctgga gaggaagtct caaagtgtcc tacaatgttg gacctggctt 600
39 tactggaaac ttttctacac aaaaagtcaa gatgcacatc cactctacca 650
40 atgaagtgac gagaatttac aatgtgatag gtactctcag aggagcagtg 700
41 gaaccagaca gatatgtcat tctgggaggt caccgggact catgggtgtt 750
42 tgggtggtatt gaccctcaga gtggagcagc tgttgttcat gaaactgtga 800
43 ggagcttttg aacactgaaa aaggaagggt ggagacctag aagaacaatt 850
44 ttgtttgcaa gctgggagtc agaagaattt ggtcttcttg gttctactga 900
45 gtgggcagag gataattcaa gactccttca agagcgtggc gtggcttata 950
46 ttaatctgta ctcatctata gaaggaaact acactctgag agttgattgt 1000
47 acaccactga tgtacagctt ggtatacaac ctaacaaaag agctgaaaag 1050
48 ccctgatgaa ggctttgaag gcaaatctct ttatgaaagt tggactaaaa 1100
49 aaagtccttc ccagagttc agtggcatgc ccaggataag caaattggga 1150
50 tctggaaatg attttgaggt gttcttccaa cgacttgga ttgcttcagg 1200
51 cagagcacgg tatactaaaa attgggaaac aaacaaattc agcggctatc 1250
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55 atgctgtagt ttaagaaag tatgctgaca aaatctacaa tatttctatg 1450
56 aaacatccac aggaaatgaa gacatacagt ttatcatttg attcactttt 1500
57 ttctgcagta aaaaatttta cagaaattgc ttccaagttc agcgagagac 1550
58 tccaggactt tgacaaaagc aaccaatat tgtaagaat gatgaatgat 1600
59 caactcatgt ttctggaaag agcatttatt gatccattag ggttaccaga 1650
60 cagacctttt tataggcatg tcatctatgc tccaagcagc cacaacaagt 1700
61 atgcagggga gtcattccca ggaatttatg atgctctgtt tgatattgaa 1750
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63 tgttgacgcc ttcacagtgc aggcagctgc agagactttg agtgaagtag 1850
64 cctaagagga ttctttagag actctgtatt gaatttgtgt ggtatgtcac 1900
65 tcaaagaata ataatgggta tattgataaa ttttaaaatt ggtatatttg 1950
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69 <210> SEQ ID NO: 2
70 <211> LENGTH: 442
71 <212> TYPE: PRT
72 <213> ORGANISM: Homo sapiens
74 <220> FEATURE:
75 <223> OTHER INFORMATION: deduced amino acid sequence of PSMA-like
76 protein
78 <400> SEQUENCE: 2
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83 Thr Gln Lys Val Lys Met His Ile His Ser Thr Asn Glu Val Thr
84 35 40 45
85 Arg Ile Tyr Asn Val Ile Gly Thr Leu Arg Gly Ala Val Glu Pro
86 50 55 60
87 Asp Arg Tyr Val Ile Leu Gly Gly His Arg Asp Ser Trp Val Phe
88 65 70 75
89 Gly Gly Ile Asp Pro Gln Ser Gly Ala Ala Val Val His Glu Thr
90 80 85 90
91 Val Arg Ser Phe Gly Thr Leu Lys Lys Glu Gly Trp Arg Pro Arg
92 95 100 105
93 Arg Thr Ile Leu Phe Ala Ser Trp Asp Ala Glu Glu Phe Gly Leu
94 110 115 120
95 Leu Gly Ser Thr Glu Trp Ala Glu Asp Asn Ser Arg Leu Leu Gln
96 125 130 135
97 Glu Arg Gly Val Ala Tyr Ile Asn Ala Asp Ser Ser Ile Glu Gly
98 140 145 150
99 Asn Tyr Thr Leu Arg Val Asp Cys Thr Pro Leu Met Tyr Ser Leu
100 155 160 165
101 Val Tyr Asn Leu Thr Lys Glu Leu Lys Ser Pro Asp Glu Gly Phe
102 170 175 180
103 Glu Gly Lys Ser Leu Tyr Glu Ser Trp Thr Lys Lys Ser Pro Ser
104 185 190 195
105 Pro Glu Phe Ser Gly Met Pro Arg Ile Ser Lys Leu Gly Ser Gly

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106	200	205	210
107	Asn Asp Phe Glu Val Phe Phe Gln Arg Leu Gly Ile Ala Ser Gly		
108	215	220	225
109	Arg Ala Arg Tyr Thr Lys Asn Trp Glu Thr Asn Lys Phe Ser Gly		
110	230	235	240
111	Tyr Pro Leu Tyr His Ser Val Tyr Glu Thr Tyr Glu Leu Val Glu		
112	245	250	255
113	Lys Phe Tyr Asp Pro Met Phe Lys Tyr His Leu Thr Val Ala Gln		
114	260	265	270
115	Val Arg Gly Gly Met Val Phe Glu Leu Ala Asn Ser Ile Val Leu		
116	275	280	285
117	Pro Phe Asp Cys Arg Asp Tyr Ala Val Val Leu Arg Lys Tyr Ala		
118	290	295	300
119	Asp Lys Ile Tyr Asn Ile Ser Met Lys His Pro Gln Glu Met Lys		
120	305	310	315
121	Thr Tyr Ser Leu Ser Phe Asp Ser Leu Phe Ser Ala Val Lys Asn		
122	320	325	330
123	Phe Thr Glu Ile Ala Ser Lys Phe Ser Glu Arg Leu Gln Asp Phe		
124	335	340	345
125	Asp Lys Ser Asn Pro Ile Leu Leu Arg Met Met Asn Asp Gln Leu		
126	350	355	360
127	Met Phe Leu Glu Arg Ala Phe Ile Asp Pro Leu Gly Leu Pro Asp		
128	365	370	375
129	Arg Pro Phe Tyr Arg His Val Ile Tyr Ala Pro Ser Ser His Asn		
130	380	385	390
132	Lys Tyr Ala Gly Glu Ser Phe Pro Gly Ile Tyr Asp Ala Leu Phe		
133	395	400	405
134	Asp Ile Glu Ser Lys Val Asp Pro Ser Lys Ala Trp Gly Asp Val		
135	410	415	420
136	Lys Arg Gln Ile Ser Val Ala Ala Phe Thr Val Gln Ala Ala Ala		
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142 <210> SEQ ID NO: 3

143 <211> LENGTH: 2653

144 <212> TYPE: DNA

145 <213> ORGANISM: Homo sapiens

147 <220> FEATURE:

148 <223> OTHER INFORMATION: nucleotide sequence of human PSMA gene

150 <300> PUBLICATION INFORMATION:

151 <308> DATABASE ACCESSION NO: GenBank Accession No. M99487

152 <309> DATABASE ENTRY DATE: 1995-01-08

154 <400> SEQUENCE: 3

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157	aactggaccc	caggtctgga	gcgaattcca	gcctgcagg	ctgataagcg	150
158	aggcattagt	gagattgaga	gagactttac	cccgcctgg	tggttgagg	200
159	gcgcgcagta	gagcagcagc	acaggcgcgg	gtcccgggag	gccggctctg	250
160	ctcgcgccga	gatgtggaat	ctccttcacg	aaaccgactc	ggctgtggcc	300

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163 atgaagctac taacattact ccaaagcata atatgaaagc atttttggat 450
164 gaattgaaag ctgagaacat caagaagttc ttatataatt ttacacagat 500
165 accacattta gcaggaacag aacaaaactt tcagcttgca aagcaaattc 550
166 aatcccagtg gaaagaattt ggcctggatt ctgttgagct agcacattat 600
167 gatgtcctgt tgcctaccc aaataagact catcccaact acatctcaat 650
168 aattaatgaa gatggaaatg agattttcaa cacatcatta tttgaaccac 700
169 ctctctccagg atatgaaaat gtttcggata ttgtaccacc tttcagtgct 750
170 ttctctcctc aaggaatgcc agagggcgat ctagtgtatg ttaactatgc 800
171 acgaactgaa gacttcttta aattggaacg ggacatgaaa atcaattgct 850
172 ctgggaaaaat tgtaattgcc agatatggga aagttttcag aggaaataag 900
173 gttaaaaatg cccagctggc aggggccaaa ggagtcattc tctactccga 950
174 ccctgctgac tactttgctc ctggggtgaa gtcctatcca gatggttgga 1000
175 atcttcctgg aggtggtgtc cagcgtggaa atatcctaaa tctgaatggt 1050
176 gcaggagacc ctctcacacc aggttaccca gcaaatgaat atgcttatag 1100
177 gcgtggaatt gcagaggctg ttggtcttcc aagtattcct gttcatccaa 1150
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180 acctggcttt actggaaact tttctacaca aaaagtcaag atgcacatcc 1300
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182 ggagcagtg aaccagacag atatgtcatt ctgggaggtc accgggactc 1400
183 atgggtgttt ggtggtattg accctcagag tggagcagct gttgttcatt 1450
184 aaattgtgag gagctttgga aactgaaaa aggaaggggt gagacctaga 1500
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192 tgcttcaggc agagcacggt atactaaaaa ttgggaaaca aacaaattca 1900
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198 ttcaactttt tctgcagtaa agaattttac agaaattgct tccaagttca 2200
199 gtgagagact ccaggacttt gacaaaagca acccaatagt attaagaatg 2250
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201 gttaccagac aggccttttt ataggcatgt catctatgct ccaagcagcc 2350
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205 gtgaagttag ctaagaggat tctttagaga atccgtattg aatttgtgtg 2550
206 gtatgtcact cagaaagaat cgtaatgggt atattgataa attttaaaat 2600
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208 aaa 2653
211 <210> SEQ ID NO: 4

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212 <211> LENGTH: 750
213 <212> TYPE: PRT
214 <213> ORGANISM: Homo sapiens
216 <220> FEATURE:
217 <223> OTHER INFORMATION: deduced amino acid sequence of PSMA protein
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225                               35          40          45
226 Ser Asn Glu Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala
227                               50          55          60
228 Phe Leu Asp Glu Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu Tyr
229                               65          70          75
230 Asn Phe Thr Gln Ile Pro His Leu Ala Gly Thr Glu Gln Asn Phe
231                               80          85          90
232 Gln Leu Ala Lys Gln Ile Gln Ser Gln Trp Lys Glu Phe Gly Leu
233                               95         100         105
234 Asp Ser Val Glu Leu Ala His Tyr Asp Val Leu Leu Ser Tyr Pro
235                               110        115        120
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237                               125        130        135
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239                               140        145        150
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241                               155        160        165
242 Pro Gln Gly Met Pro Glu Gly Asp Leu Val Tyr Val Asn Tyr Ala
243                               170        175        180
244 Arg Thr Glu Asp Phe Phe Lys Leu Glu Arg Asp Met Lys Ile Asn
245                               185        190        195
246 Cys Ser Gly Lys Ile Val Ile Ala Arg Tyr Gly Lys Val Phe Arg
247                               200        205        210
248 Gly Asn Lys Val Lys Asn Ala Gln Leu Ala Gly Ala Lys Gly Val
249                               215        220        225
250 Ile Leu Tyr Ser Asp Pro Ala Asp Tyr Phe Ala Pro Gly Val Lys
251                               230        235        240
252 Ser Tyr Pro Asp Gly Trp Asn Leu Pro Gly Gly Gly Val Gln Arg
253                               245        250        255
254 Gly Asn Ile Leu Asn Leu Asn Gly Ala Gly Asp Pro Leu Thr Pro
255                               260        265        270
256 Gly Tyr Pro Ala Asn Glu Tyr Ala Tyr Arg Arg Gly Ile Ala Glu
257                               275        280        285
258 Ala Val Gly Leu Pro Ser Ile Pro Val His Pro Ile Gly Tyr Tyr
259                               290        295        300
260 Asp Ala Gln Lys Leu Leu Glu Lys Met Gly Gly Ser Ala Pro Pro
261                               305        310        315
263 Asp Ser Ser Trp Arg Gly Ser Leu Lys Val Pro Tyr Asn Val Gly

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VERIFICATION SUMMARY

DATE: 09/11/2003

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L:10 M:270 C: Current Application Number differs, Replaced Current Application Number